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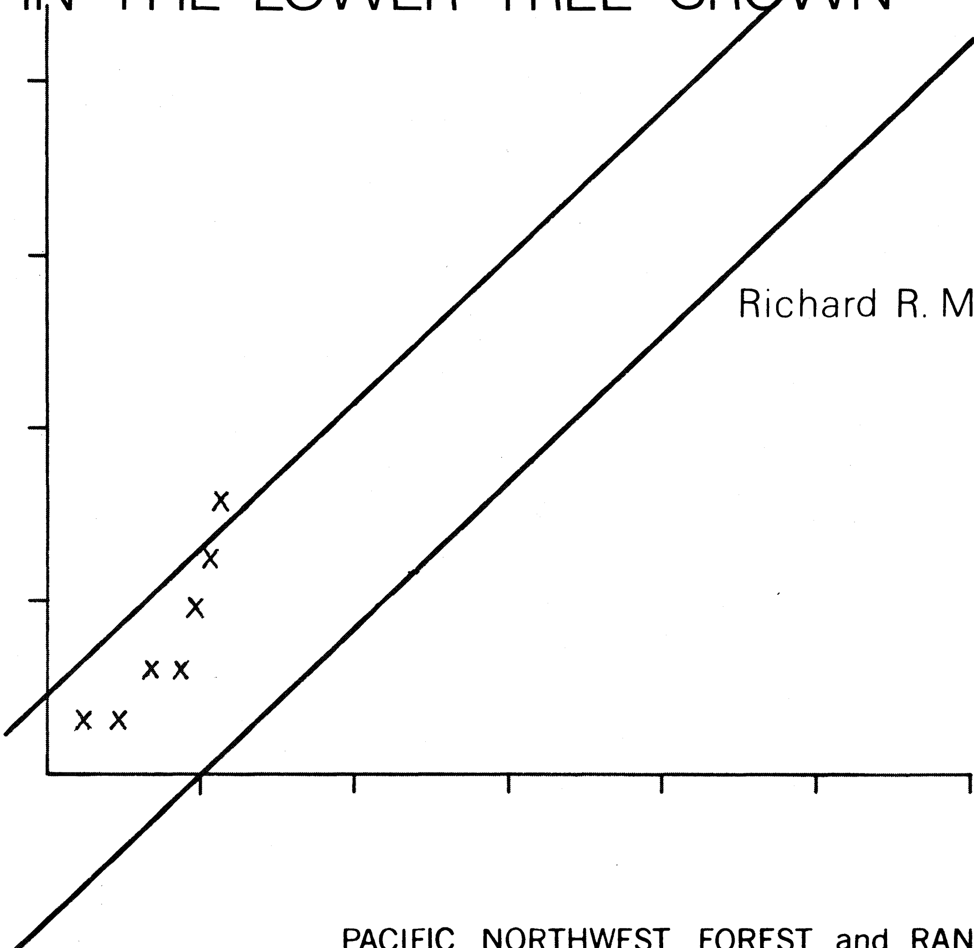
DETECTING SUBOUTBREAK POPULATIONS OF THE DOUGLAS-FIR TUSSOCK MOTH BY SEQUENTIAL SAMPLING OF EARLY LARVAE IN THE LOWER TREE CROWN



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DETECTING SUBOUTBREAK POPULATIONS OF THE DOUGLAS-FIR TUSSOCK MOTH BY SEQUENTIAL SAMPLING OF EARLY LARVAE IN THE LOWER TREE CROWN

Reference Abstract

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A sequential sampling plan is described for identifying tussock moth populations which, at a maximum expected rate of increase, could be within 1 year of outbreak status. The plan uses a new technique of sampling early larvae by the nondestructive examination of lower crown foliage. Larvae at inconspicuous low densities are classified into relatively low or high categories by their frequency of occurrence on foliage samples. The sampling plan is applied independently on individual plots to classify the density of each plot. It is an appropriate method for quickly screening suboutbreak populations in ground evaluation surveys.

KEYWORDS: Population sampling, insect populations, Douglas-fir tussock moth, *Orgyia pseudotsugata*, insect surveys.

RESEARCH SUMMARY

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Low density populations of tussock moth are usually evaluated in terms of the density of young larvae on the foliage. Estimates of larval density with a high level of precision, however, are unnecessary for most survey purposes. A general classification of density that is biologically meaningful can be substituted and is easier to determine than a precise estimate.

A rationale has been developed for classifying larval numbers, which are presently inconspicuous on the foliage, into either a low-level population which, at a maximum rate of expected increase, is at least 2 years away from causing visible tree defoliation; or a suboutbreak population which has the potential of increasing to an outbreak level in 1 year. The categories are especially useful for evaluating known populations of tussock moth suspected of having an upward trend in numbers.

A sequential sampling plan was derived for field classification of plots into either the low-level or suboutbreak category. Sampling is by nondestructive examination of the lower crown foliage of randomly selected trees on a plot. A design for a pocket tally sheet with the built-in sequential plan is also given. Using the sequential plan one person can determine the present status of a larval population on a plot with only a fraction of the amount of sampling normally required for evaluation.

Introduction

The Douglas-fir tussock moth, *Orgyia pseudotsugata* (McDunnough), is a major defoliator of Douglas-fir, *Pseudotsuga menziesii* var. *glauca* (Beissn.) Franco, and many of the true firs, *Abies* spp., in Western North America. Outbreaks erupt suddenly and often synchronously in patches over large forested areas. The early recognition of impending outbreak conditions is essential for planning control activities to prevent tree damage during the 1st year of heavy defoliation (Wickman 1978).

Low-density populations of the Douglas-fir tussock moth do not cause tree defoliation that can be detected by aerial observation; therefore, preoutbreak numbers can only be evaluated from the ground by trapping male moths or examining foliage for other life stages. A standard criterion for ground evaluation is the density of young larvae (1st-2d instars) newly established on the foliage in the spring or early summer. Methods have been developed for making precise estimates of density by sampling foliage from branches in the middle portion of the tree and expressing the number of larvae in terms of 1,000 square inches[1] of branch area (Mason 1970). Midcrown foliage is usually sampled by clipping 46-cm (18-in) branches with a pole-pruner and collecting the samples in a basket attached to the pole. This method has recently been modified for low-density populations by a nondestructive sampling technique relating density in the lower crown to density in the standard midcrown (Mason 1977). Such methods of estimating density, however, are time consuming and usually impractical for conducting large scale ground surveys.

Estimates of larval density with high levels of precision are often not necessary to evaluate population status. This is especially true for low densities which, even at a potentially maximum rate of population growth, may be more than 1 year away from an outbreak level. In such cases, the classification of larval densities on sample plots into biologically meaningful categories may be the only information needed from the initial survey. Sequential sampling is particularly appropriate for these situations because population densities are only classified, usually at a considerable saving in time and effort over conventional sampling methods. If additional detail is required for plots in a particular density class, estimates with a desired level of precision can still be made after populations in that class have been screened by the sequential survey.

Sequential analysis was first developed during World War II as a rapid method for making statistical evaluations (Statistical Research Group, Columbia University 1957; Wald 1947). Its value in biology was quickly recognized, and the method was soon recommended for conducting forest insect surveys (Oakland 1951, Stark 1952, Waters 1955). Sequential sampling plans for classifying populations have since been prepared for a variety of forest insects (Waters 1974). Plans are also available for classifying eggs and larvae of the Douglas-fir tussock moth by destructive sampling of branches (Mason 1969). Methods of constructing sequential plans and their uses in pest management have been adequately described by Onsager (1976) and Waters (1955). In this paper a sequential sampling plan is given for rapid identification of low-density populations of tussock moth larvae that may be only one generation removed from an outbreak level. Sampling is done by nondestructive examination of foliage in the lower tree crown.

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[1]Metric equivalent of 1,000 in^2 is 0.6452 m^2.

Rationale for Population Density Classes

Tree defoliation by the tussock moth is not usually conspicuous until the average population density reaches about 20 early instars per 1,000 in^2, although higher densities are required to cause significant tree damage (Wickman 1978). Populations which attain the threshold density where defoliation is easily visible have traditionally been called "outbreaks." During the years of population increase preceding an outbreak, the maximum multiplication rate between generations is usually less than 10 and has averaged about 7 for the infestations studied in detail (Mason 1974; in press). At an annual multiplication rate of 7, therefore, populations with an average density of small larvae $\geq 20/1{,}000$ in^2 must have a density $\geq 3.0/1{,}000$ in^2 1 year before the first visible defoliation. Populations with densities $\leq 1.0/1{,}000$ in^2 are at least 2 years away from causing visible defoliation. In other words, low-density populations $\geq 3.0/1{,}000$ in^2 could be in a release year; i.e., they have the potential of reaching outbreak status by the next generation if they have the maximum expected rate of increase. Population densities $\leq 1.0/1{,}000$ in^2, on the other hand, have only a slight chance of becoming an outbreak for at least 2 years.

The above threshold densities are useful for evaluating results from ground surveys because they identify populations that could be entering a release phase of an outbreak and separate them from populations that are still at a relatively insignificant level. Therefore, these thresholds were set as the class limits in a two-class sequential plan. Two hypotheses for the plan are

H_1: $M \leq 1.0$ larva/1,000 in^2; i.e., *low-level* population at least 2 or more years away from outbreak; and

H_2: $M \geq 3.0$ larvae/1,000 in^2; i.e., *suboutbreak* population potentially 1 year away from outbreak;

where

M = mean number of larvae/1,000 in^2 of branch area in the midcrown.

The Primary Sample Unit

All sampling is done on lower branches of trees within reach from the ground. The primary sample unit is three 46- to 56-cm (18- to 22-in) branches per tree examined in place by rapping each with a stick over a hand-held drop cloth. Larvae that drop from the foliage are easily observed on the cloth. A drop cloth of dimensions of 61 by 122 cm (24 by 48 in) supported underneath at the corners by a pair of cross sticks has been used satisfactorily.

The proportion of primary sample units that are infested (i.e., one or more larvae per sample unit) is an adequate index of the standard midcrown density (Mason 1977). Midcrown density of 1st and 2d instars can be estimated from the frequency of occurrence of larvae on lower crown sample units by

$$\hat{M} = -4 \ln(1-p);$$

where

$\hat{M}$ = estimate of M and

p = the true proportion of lower crown sample units that are infested.

Class limits designated for the sequential plan can be expressed in terms of the proportion of primary sample units infested by substituting and solving for p in the above equation (fig. 1). The hypotheses

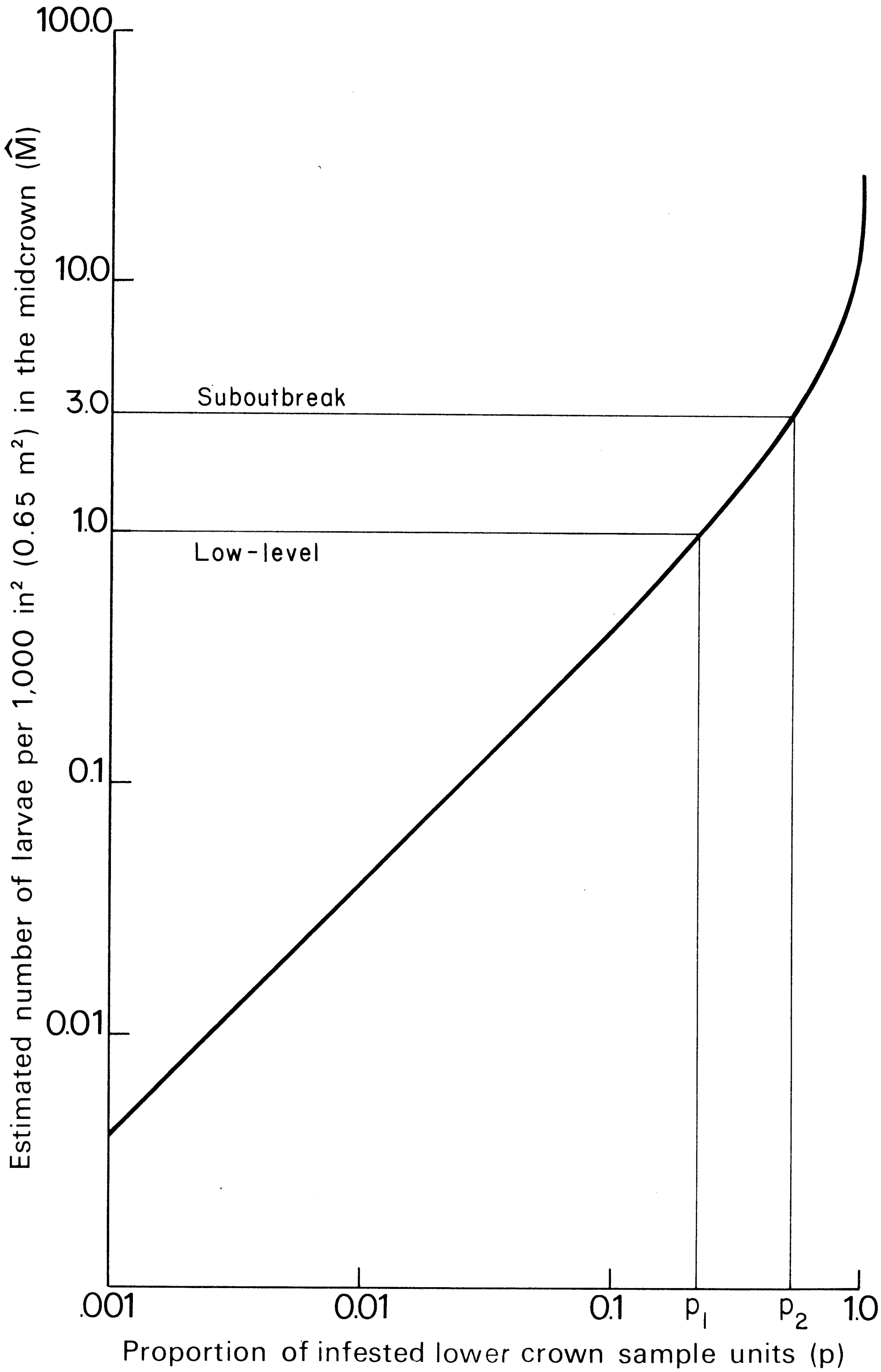

Figure 1.--Relationship of midcrown density to proportion of infested lower crown sample units plotted on logarithmic scale (modified from Mason 1977).

stated in terms of p then become

$H_1 : p \leq 0.2212$ and
$H_2 : p \geq 0.5276$.

The parameter p is estimated by the presence or absence of larvae on sample units; therefore, the binomial distribution, which assumes that every sample unit has an equal probability of being infested, is used for calculating the sequential plan.

Sequential Decision Plan

Construction of the sequential plan requires selection of risk levels for making incorrect decisions. These are usually referred to as alpha (α), the risk of rejecting a hypothesis when it is true, and beta (β), the risk of accepting a hypothesis when it is false. In this plan both allowable risks were set at 0.05 which means the maximum chance of mislabeling a population is 1 in 20.

Two parallel decision lines are used for testing the formulated hypotheses. These are calculated according to the equation for a straight line,

$$d_{1,2} = bn \pm a_{1,2} ;$$

where

d = cumulative number of infested sample units,

n = total number of trees sampled,

b = slope of the lines, and

a = the Y-intercept.

The slope and intercepts were calculated from the general formulas below given by Waters (1955) for sampling a binomial distribution.

Slope:

$$b = \frac{\log\left(\frac{1-p_1}{1-p_2}\right)}{\log \frac{p_2}{p_1}\left(\frac{1-p_1}{1-p_2}\right)} .$$

Intercepts:

$$a_1 = \frac{\log\left(\frac{1-\alpha}{\beta}\right)}{\log \frac{p_2}{p_1}\left(\frac{1-p_1}{1-p_2}\right)} ;$$

$$a_2 = \frac{\log\left(\frac{1-\beta}{\alpha}\right)}{\log \frac{p_2}{p_1}\left(\frac{1-p_1}{1-p_2}\right)} ;$$

where

p_1 = the proportion specified as the upper limit of the lower-level class (H_1), and

p_2 = the proportion specified as the lower limit of the suboutbreak class (H_2).

After solving for the slope and intercepts, the equations for the two decision lines are:

$$d_1 = 0.365n - 2.151 \text{ (lower line)};$$

$$d_2 = 0.365n + 2.151 \text{ (upper line)}.$$

These lines are plotted in figure 2 which represents the sequential decision plan for testing hypotheses H_1 and H_2. If the cumulative number of infested sample units falls below the lower line for a given random sample of trees, H_1 is accepted and the tussock moth population is classified "low-level." If the cumulative number of infested units is above the upper line for the number of sampled trees, H_2 is accepted and the population is classified "suboutbreak." Intermediate values of infested sample units require that random sampling of trees continue until a decision line is crossed. If no decision is reached, the plan may call for sampling to be truncated after some arbitrary number of trees has been examined and the population is classified "intermediate."

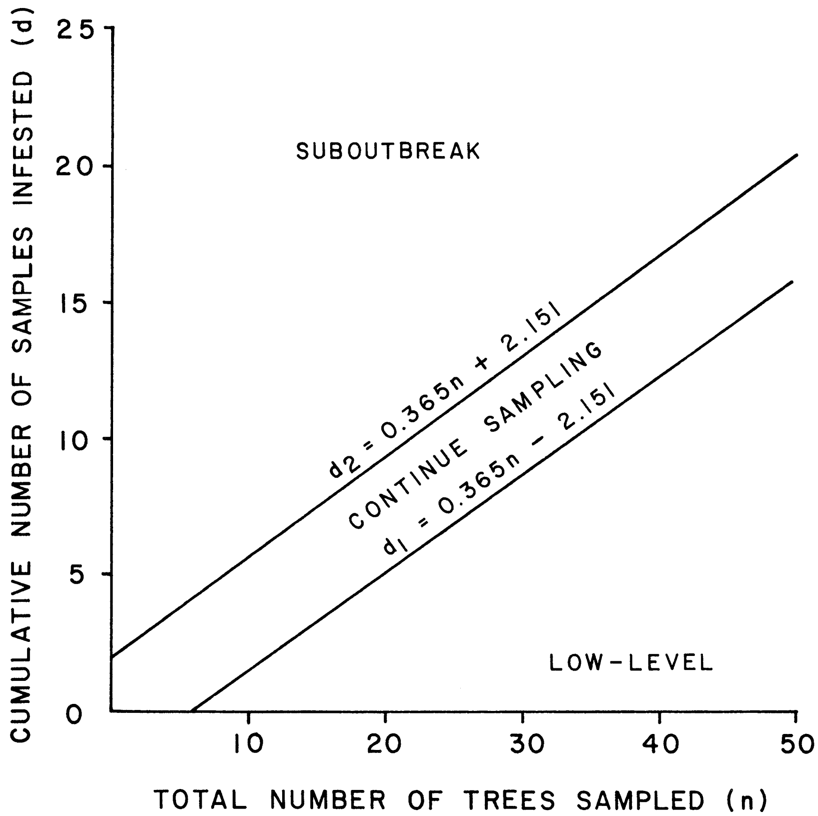

Figure 2.--Sequential graph for sampling early larvae of the Douglas-fir tussock moth in the lower tree crown.

Performance of the sequential plan can be evaluated in advance of actual sampling from the operating characteristic (OC) and average sample number (ASN) curves. These have been calculated from formulas published by the Statistical Research Group, Columbia University (1957) and are plotted in figure 3. Similar formulas for calculating OC and ASN curves are given by Waters (1955) and Onsager (1976).

The OC curve shows the probability of accepting H_1 for different values of p. If $p = p_1 = 0.22$ which is the upper class limit for a low-level population, the probability of accepting H_1 is 0.95 and the probability of rejection (α) is 0.05. The chance of accepting H_1 for lower values of p is even higher than 0.95. Conversely, if $p = p_2 = 0.53$ which is the lower limit of a suboutbreak population, the probability of accepting H_1 is 0.05 (β) and the probability of rejection is 0.95. The risk of classifying a population density >3.0/1,000 in^2 as anything but "suboutbreak" is very small. Intermediate densities are more difficult to classify--such as a density of 1.8 larvae/1,000 in^2 ($p = 0.36$) which has an equal chance of classification in either category.

The ASN curve shows the average number of trees that need to be examined to reach a decision. The fewest trees are needed for densities within the class limits and the most trees for

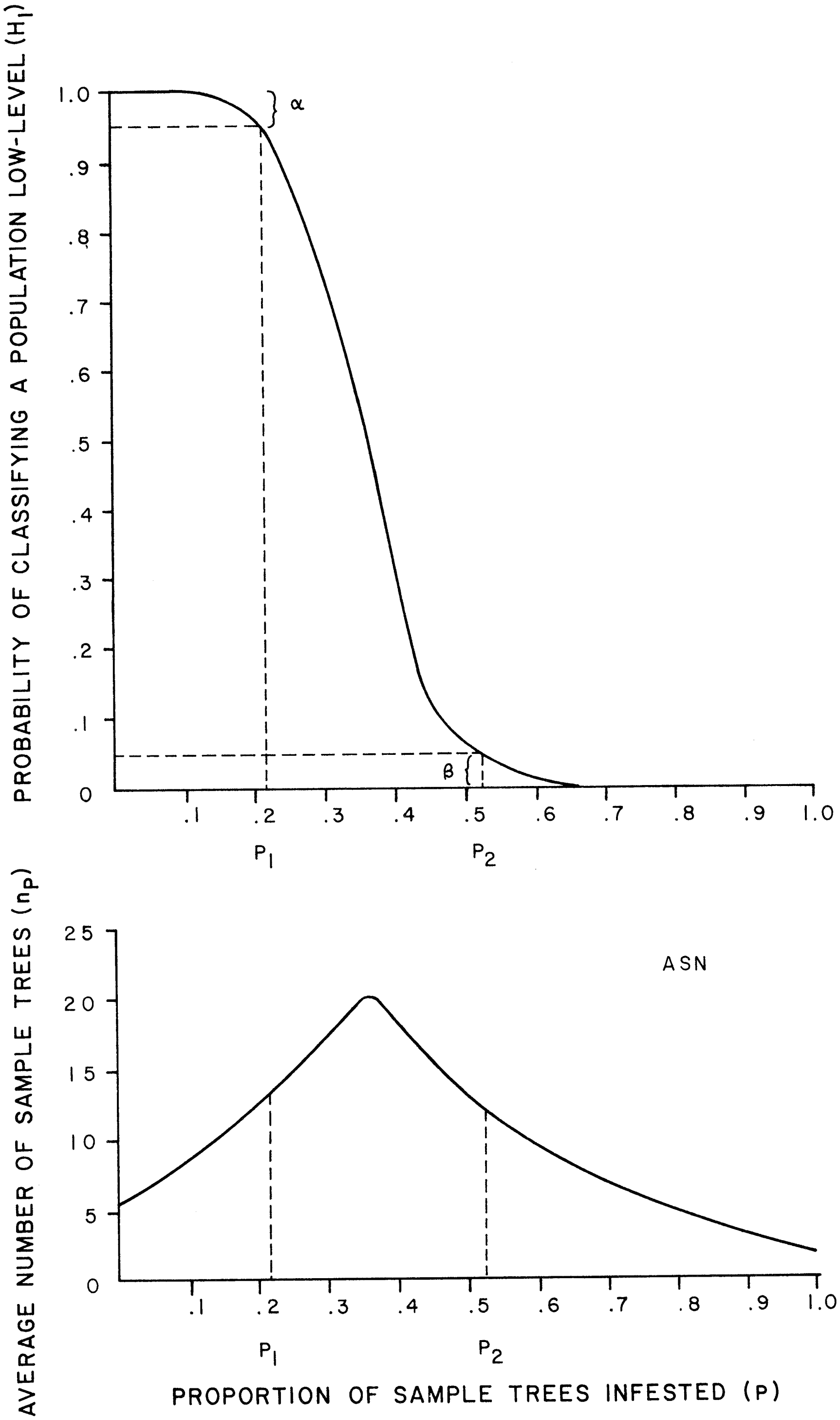

Figure 3.--Operating characteristic (OC) and average sample number (ASN) curves for sequential sampling early larvae in the lower crown.

intermediate densities. Obviously, the greatest savings from use of the sequential plan come from sampling larval densities clearly in one class or the other and the least savings from borderline densities.

Field Use of the Plan

An underlying assumption in sequential analysis is that sample trees have been selected randomly; i.e., each tree on the plot where the insect population is being evaluated has an equal chance of being chosen. If a plot is about 2 ha (4.9 acres) in size, then each eligible tree in that 2 ha is assumed to have an equal chance of being selected for the sample. This theoretical assumption can be satisfied in the field by using a randomized procedure, such as a random numbers table or rolling dice, to determine the direction and distance between successive sample trees. For example, after one tree has been sampled, the direction (azimuth) and distance to the next tree is quickly determined from two random numbers. Units of measure can be scaled so that sample trees are sure to fall within the plot area. Trees might also be selected by gridding the plot on paper and randomly choosing coordinates to locate sampling spots. Because decisions of classification are based on sample units chosen at random and examined in sequence, trees must be sampled in order of their random selection and not by the shortest travel route between trees.

Trees selected for sampling need at least three lower branches suitable for the sample unit. Such branches must be well foliated and current needles available to feeding larvae; otherwise they would not be an acceptable habitat for early instars.

Graphs or tables with the sequential plan are awkward to use in the field. A field tally sheet which incorporates the calculated numerical values of the sequential plan is illustrated in figure 4. This sheet can be conveniently carried by a sampler in a pocket-size tally book; this leaves both hands free for holding the drop cloth and rapping stick. The class limits for decisionmaking are printed in the squares across the top of the columns for the number of trees sampled. The top left corner gives the upper limit of a "low-level" population and the bottom right corner the lower limit of a "suboutbreak" population.

As trees are sampled on each plot, the number of primary sample units that are infested is accumulated across the page. When the cumulative total equals or is less than the top value in the overhead box, sampling is terminated and the plot is classified "low-level" (e.g., plots A and B in fig. 4). When the cumulative total equals or is more than the bottom value, the plot is classified "suboutbreak" (e.g., plots C and D). If a decision is not reached after 20 trees, sampling is terminated and the plot classified "intermediate" (e.g., plot E).

Time of sampling is particularly important because the sequential plan is based on an evaluation when the majority of larvae are expected to be in the first instar, having only recently dispersed from hatched eggs onto new foliage. Sampling too early or too late will result in an inaccurate survey. Unfortunately, considerable variation occurs in the time of egg hatch and dispersal of larvae because of seasonal and physiographic differences. Wickman (1976a, 1976b) found that egg hatch and larval development are closely related to tree phenology and that sampling for small larvae can be properly timed by observing shoot development. In Oregon and California, the proper time for sampling newly established small larve is when all buds on host species have burst and average growth of new shoots has reached 1 to 2 inches.

PLOTS	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	CLASS	REMARKS
	LOW / SUB			-/4	-/4	0/5	0/5	0/6	1/6	1/6	1/7	2/7	2/7	2/8	3/8	3/8	4/9	4/9	4/10	5/10		
A	0	0	0	0	0	0															L	
B	0	0	0	1	1	1	2	2	3	3	3	3	3	3	3						L	
C	1	2	3	4																	S	
D	0	1	1	2	3	3	3	4	4	5	6	6	7								S	
E	0	0	1	1	1	1	2	2	3	3	3	3	4	4	5	5	5	5	5	6	I	

Figure 4.--Field tally sheet with examples for sequential sampling early larvae of the Douglas-fir tussock moth.

Discussion

This sequential plan is not intended for a single evaluation of a large forest area. Instead, it is recommended simply as a quick substitute for precise sampling on individual plots expected to have a relatively homogenous population. The number of plots needed to evaluate a large area will depend on numerous considerations including the design and purpose of the survey, distribution of habitat types, and variability in the insect population.

Acceptance of H_2 and the classification of a suboutbreak density are not a prediction of an outbreak but are only an identification of a density level of early instars having the potential to increase to an outbreak level in a single generation. Whether or not rapid population growth takes place depends on survivorship of subsequent life stages in that generation and the early part of the next generation. Such general survey information is most valuable for alerting managers to potential outbreak situations so that they can make a more reliable prognosis from followup evaluations.

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